

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/562,472
Source: PCT
Date Processed by STIC: 01/12/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/562, 472

CRF Edit Date: 01/12/2006
Edited by: DA

___ **Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line**

___ **Corrected the SEQ ID NO. Sequence numbers edited were:**

___ **Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:**

✓ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ **Inserted mandatory headings/numeric identifiers, specifically:**

___ **Moved responses to same line as heading/numeric identifier, specifically:**

___ **Other:**



PCT

RAW SEQUENCE LISTING

DATE: 01/12/2006

PATENT APPLICATION: US/10/562,472

TIME: 11:42:48

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01122006\J562472.raw

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4 <110> APPLICANT: Bayer CropScience AG
6 <120> TITLE OF INVENTION: Method of identifying fungicidally active compounds based on
fungal
7     mevalonate kinases
9 <130> FILE REFERENCE: BCS 03-3035
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/562,472
C--> 11 <141> CURRENT FILING DATE: 2005-12-22
11 <160> NUMBER OF SEQ ID NOS: 2
13 <170> SOFTWARE: PatentIn version 3.1
15 <210> SEQ ID NO: 1
17 <211> LENGTH: 1341
19 <212> TYPE: DNA
21 <213> ORGANISM: Ustilago maydis
23 <220> FEATURE:
25 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1341)
29 <223> OTHER INFORMATION:
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34 Met Asn Arg Ala Arg Leu Glu Thr Arg Gly Gly Glu Gly Glu Pro Arg
35 1             5             10             15
37 tcg gct cag gat cac ccg ccg ccg tcg tcg gtg gtt gtc agt gcg cct      96
38 Ser Ala Gln Asp His Pro Pro Pro Ser Ser Val Val Val Ser Ala Pro
39             20             25             30
41 ggc aag gtg atc ctt ttc ggt gag cac gca gtg gtg cat ggt att act      144
42 Gly Lys Val Ile Leu Phe Gly Glu His Ala Val Val His Gly Ile Thr
43             35             40             45
45 gct gtc gcc gcc tcg gtg gcg ctg cga tgc tac gct aac gta tcg cca      192
46 Ala Val Ala Ala Ser Val Ala Leu Arg Cys Tyr Ala Asn Val Ser Pro
47             50             55             60
49 cga gag gat ggc aag att tcg ctc gat ttg cct gat ctc ggc gtg atc      240
50 Arg Glu Asp Gly Lys Ile Ser Leu Asp Leu Pro Asp Leu Gly Val Ile
51 65             70             75             80
53 cac act tgg aac atc gcc gat ctt cct tgg tct gct gtg cct aaa tcc      288
54 His Thr Trp Asn Ile Ala Asp Leu Pro Trp Ser Ala Val Pro Lys Ser
55             85             90             95
57 att caa ggt ggt ggc gcc gta cct gac tcg ctc gac aag acg ctt att      336
58 Ile Gln Gly Gly Gly Ala Val Pro Asp Ser Leu Asp Lys Thr Leu Ile
59             100            105            110
61 ggc gcc atc gaa aag gtg gtg ggc gac acg gtc aac gag agc gaa aga      384
62 Gly Ala Ile Glu Lys Val Val Gly Asp Thr Val Asn Glu Ser Glu Arg
63             115            120            125
65 agc cat gct gct tcg atc gcc ttt ctg gtg ctt tac atg tgc atc gcc      432
66 Ser His Ala Ala Ser Ile Ala Phe Leu Val Leu Tyr Met Cys Ile Ala

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67	130	135	140	
69	ggt cag gct gat gcg cgc gct cag gca ttt gtg ctg cgt tcg gct ctg	480		
70	Gly Gln Ala Asp Ala Arg Ala Gln Ala Phe Val Leu Arg Ser Ala Leu			
71	145 150 155 160			
73	ccc atc ggt gca gga ctc ggc tca agc gcc gcg ctc agc tcg tgc ctc	528		
74	Pro Ile Gly Ala Gly Leu Gly Ser Ser Ala Ala Leu Ser Ser Cys Leu			
75	165 170 175			
77	gct gcg gcg ctc acc atc ctc tat ggt cgc att ccc gct ccg ggc agc	576		
78	Ala Ala Ala Leu Thr Ile Leu Tyr Gly Arg Ile Pro Ala Pro Gly Ser			
79	180 185 190			
81	gaa ctg tca gct gag cac tcg aca cac atc aac gaa tgg gcc ttt ttg	624		
82	Glu Leu Ser Ala Glu His Ser Thr His Ile Asn Glu Trp Ala Phe Leu			
83	195 200 205			
85	tct gaa aag gta att cac ggc acc ccc tcg ggt gtt gac aac acg gtg	672		
86	Ser Glu Lys Val Ile His Gly Thr Pro Ser Gly Val Asp Asn Thr Val			
87	210 215 220			
89	gct gtt cat ggc gga gcg atc gct ttc act cgt gct cac cca agc aac	720		
90	Ala Val His Gly Gly Ala Ile Ala Phe Thr Arg Ala His Pro Ser Asn			
91	225 230 235 240			
93	acg ctc aca gcc aac aag atg aac aag ctc aaa ggc ttc tct tcg ttc	768		
94	Thr Leu Thr Ala Asn Lys Met Asn Lys Leu Lys Gly Phe Ser Ser Phe			
95	245 250 255			
97	cgt ttc ctc ctc gtc gac agc tgc gtc ggc cgc gag ggc aag aag ctg	816		
98	Arg Phe Leu Leu Val Asp Ser Cys Val Gly Arg Glu Gly Lys Lys Leu			
99	260 265 270			
101	atc gct cac gtt gca gct cag aag gaa tcc gag ccg act cgt gtc aat	864		
102	Ile Ala His Val Ala Ala Gln Lys Glu Ser Glu Pro Thr Arg Val Asn			
103	275 280 285			
105	gcg gct ctc gct cga atc cag acg atc gcc gat tcg gcc cag ctc gtg	912		
106	Ala Ala Leu Ala Arg Ile Gln Thr Ile Ala Asp Ser Ala Gln Leu Val			
107	290 295 300			
109	ctc act ggc aac tcg ggt ctc tct cgc tcc gag caa gtt gca cag ctt	960		
110	Leu Thr Gly Asn Ser Gly Leu Ser Arg Ser Glu Gln Val Ala Gln Leu			
111	305 310 315 320			
113	cgc gaa ctg atc aag cag aac cat agc gaa ctt gtt ggg ctc gag gta	1008		
114	Arg Glu Leu Ile Lys Gln Asn His Ser Glu Leu Val Gly Leu Glu Val			
115	325 330 335			
117	tcg cac gct tcg ctg gag ttg atc aag aac aag acc gag tcg ttt gca	1056		
118	Ser His Ala Ser Leu Glu Leu Ile Lys Asn Lys Thr Glu Ser Phe Ala			
119	340 345 350			
121	ccc gat cag ctg gct act aag ctc aca ggt gcc gga gga gga gga tgt	1104		
122	Pro Asp Gln Leu Ala Thr Lys Leu Thr Gly Ala Gly Gly Gly Cys			
123	355 360 365			
125	gca gtt aca ctg ctg ccg gac gac ttt gag gag gag aag gtg aag gag	1152		
126	Ala Val Thr Leu Leu Pro Asp Asp Phe Glu Glu Glu Lys Val Lys Glu			
127	370 375 380			
129	ctg atg agc gag ctg gag aat gct ggc ttt aag tgc tac gag acc aga	1200		
130	Leu Met Ser Glu Leu Glu Asn Ala Gly Phe Lys Cys Tyr Glu Thr Arg			
131	385 390 395 400			

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133 gtg gga ggt gac ggc ttc ggc gtc aag ctt ctg cag gac gaa cag gag      1248
134 Val Gly Gly Asp Gly Phe Gly Val Lys Leu Leu Gln Asp Glu Gln Glu
135                               405                               410                               415
137 gag gcc gag gcc aag ctg cga ttc aag gaa gcc aac gtg agc aac gag      1296
138 Glu Ala Glu Ala Lys Leu Arg Phe Lys Glu Ala Asn Val Ser Asn Glu
139                               420                               425                               430
141 ctg gct gtg tgg gct gat gag ctt gct ggt tgg gta ttt gcc tga      1341
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143                               435                               440                               445
146 <210> SEQ ID NO: 2
148 <211> LENGTH: 446
150 <212> TYPE: PRT
152 <213> ORGANISM: Ustilago maydis
154 <400> SEQUENCE: 2
157 Met Asn Arg Ala Arg Leu Glu Thr Arg Gly Gly Glu Gly Glu Pro Arg
158 1                               5                               10                               15
161 Ser Ala Gln Asp His Pro Pro Pro Ser Ser Val Val Val Ser Ala Pro
162                               20                               25                               30
165 Gly Lys Val Ile Leu Phe Gly Glu His Ala Val Val His Gly Ile Thr
166                               35                               40                               45
169 Ala Val Ala Ala Ser Val Ala Leu Arg Cys Tyr Ala Asn Val Ser Pro
170                               50                               55                               60
173 Arg Glu Asp Gly Lys Ile Ser Leu Asp Leu Pro Asp Leu Gly Val Ile
174 65                               70                               75                               80
177 His Thr Trp Asn Ile Ala Asp Leu Pro Trp Ser Ala Val Pro Lys Ser
178                               85                               90                               95
181 Ile Gln Gly Gly Gly Ala Val Pro Asp Ser Leu Asp Lys Thr Leu Ile
182                               100                              105                              110
185 Gly Ala Ile Glu Lys Val Val Gly Asp Thr Val Asn Glu Ser Glu Arg
186                               115                              120                              125
189 Ser His Ala Ala Ser Ile Ala Phe Leu Val Leu Tyr Met Cys Ile Ala
190                               130                              135                              140
193 Gly Gln Ala Asp Ala Arg Ala Gln Ala Phe Val Leu Arg Ser Ala Leu
194 145                              150                              155                              160
197 Pro Ile Gly Ala Gly Leu Gly Ser Ser Ala Ala Leu Ser Ser Cys Leu
198                               165                               170                               175
201 Ala Ala Ala Leu Thr Ile Leu Tyr Gly Arg Ile Pro Ala Pro Gly Ser
202                               180                               185                               190
205 Glu Leu Ser Ala Glu His Ser Thr His Ile Asn Glu Trp Ala Phe Leu
206                               195                               200                               205
209 Ser Glu Lys Val Ile His Gly Thr Pro Ser Gly Val Asp Asn Thr Val
210                               210                               215                               220
213 Ala Val His Gly Gly Ala Ile Ala Phe Thr Arg Ala His Pro Ser Asn
214 225                              230                              235                              240
217 Thr Leu Thr Ala Asn Lys Met Asn Lys Leu Lys Gly Phe Ser Ser Phe
218                               245                               250                               255
221 Arg Phe Leu Leu Val Asp Ser Cys Val Gly Arg Glu Gly Lys Lys Leu
222                               260                               265                               270
225 Ile Ala His Val Ala Ala Gln Lys Glu Ser Glu Pro Thr Arg Val Asn

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226          275          280          285
229 Ala Ala Leu Ala Arg Ile Gln Thr Ile Ala Asp Ser Ala Gln Leu Val
230          290          295          300
233 Leu Thr Gly Asn Ser Gly Leu Ser Arg Ser Glu Gln Val Ala Gln Leu
234 305          310          315          320
237 Arg Glu Leu Ile Lys Gln Asn His Ser Glu Leu Val Gly Leu Glu Val
238          325          330          335
241 Ser His Ala Ser Leu Glu Leu Ile Lys Asn Lys Thr Glu Ser Phe Ala
242          340          345          350
245 Pro Asp Gln Leu Ala Thr Lys Leu Thr Gly Ala Gly Gly Gly Cys
246          355          360          365
249 Ala Val Thr Leu Leu Pro Asp Asp Phe Glu Glu Glu Lys Val Lys Glu
250          370          375          380
253 Leu Met Ser Glu Leu Glu Asn Ala Gly Phe Lys Cys Tyr Glu Thr Arg
254 385          390          395          400
257 Val Gly Gly Asp Gly Phe Gly Val Lys Leu Leu Gln Asp Glu Gln Glu
258          405          410          415
261 Glu Ala Glu Ala Lys Leu Arg Phe Lys Glu Ala Asn Val Ser Asn Glu
262          420          425          430
265 Leu Ala Val Trp Ala Asp Glu Leu Ala Gly Trp Val Phe Ala
266          435          440          445

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/562,472

DATE: 01/12/2006

TIME: 11:42:49

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01122006\J562472.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:31 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29

**Raw Sequence Listing before editing
(for reference only)**



PCT

RAW SEQUENCE LISTING

DATE: 01/09/2006

PATENT APPLICATION: US/10/562,472

TIME: 11:29:40

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01092006\J562472.raw

4 <110> APPLICANT: Bayer CropScience AG
 6 <120> TITLE OF INVENTION: Method of identifying fungicidally active compounds based on fungal
 7 mevalonate kinases
 9 <130> FILE REFERENCE: BCS 03-3035
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/562,472
 C--> 11 <141> CURRENT FILING DATE: 2005-12-22
 11 <160> NUMBER OF SEQ ID NOS: 2
 13 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
 Corrected Diskette Needed

Cpg-2)

ERRORED SEQUENCES

146 <210> SEQ ID NO: 2
 148 <211> LENGTH: 446
 150 <212> TYPE: PRT
 152 <213> ORGANISM: Ustilago maydis
 154 <400> SEQUENCE: 2
 157 Met Asn Arg Ala Arg Leu Glu Thr Arg Gly Gly Glu Gly Glu Pro Arg
 158 1 5 10 15
 161 Ser Ala Gln Asp His Pro Pro Pro Ser Ser Val Val Val Ser Ala Pro
 162 20 25 30
 165 Gly Lys Val Ile Leu Phe Gly Glu His Ala Val Val His Gly Ile Thr
 166 35 40 45
 169 Ala Val Ala Ala Ser Val Ala Leu Arg Cys Tyr Ala Asn Val Ser Pro
 170 50 55 60
 173 Arg Glu Asp Gly Lys Ile Ser Leu Asp Leu Pro Asp Leu Gly Val Ile
 174 65 70 75 80
 177 His Thr Trp Asn Ile Ala Asp Leu Pro Trp Ser Ala Val Pro Lys Ser
 178 85 90 95
 181 Ile Gln Gly Gly Gly Ala Val Pro Asp Ser Leu Asp Lys Thr Leu Ile
 182 100 105 110
 185 Gly Ala Ile Glu Lys Val Val Gly Asp Thr Val Asn Glu Ser Glu Arg
 186 115 120 125
 189 Ser His Ala Ala Ser Ile Ala Phe Leu Val Leu Tyr Met Cys Ile Ala
 190 130 135 140
 193 Gly Gln Ala Asp Ala Arg Ala Gln Ala Phe Val Leu Arg Ser Ala Leu
 194 145 150 155 160
 197 Pro Ile Gly Ala Gly Leu Gly Ser Ser Ala Ala Leu Ser Ser Cys Leu
 198 165 170 175
 201 Ala Ala Ala Leu Thr Ile Leu Tyr Gly Arg Ile Pro Ala Pro Gly Ser
 202 180 185 190
 205 Glu Leu Ser Ala Glu His Ser Thr His Ile Asn Glu Trp Ala Phe Leu
 206 195 200 205

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DATE: 01/09/2006

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TIME: 11:29:40

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01092006\J562472.raw

209 Ser Glu Lys Val Ile His Gly Thr Pro Ser Gly Val Asp Asn Thr Val
210 210 215 220
213 Ala Val His Gly Gly Ala Ile Ala Phe Thr Arg Ala His Pro Ser Asn
214 225 230 235 240
217 Thr Leu Thr Ala Asn Lys Met Asn Lys Leu Lys Gly Phe Ser Ser Phe
218 245 250 255
221 Arg Phe Leu Leu Val Asp Ser Cys Val Gly Arg Glu Gly Lys Lys Leu
222 260 265 270
225 Ile Ala His Val Ala Ala Gln Lys Glu Ser Glu Pro Thr Arg Val Asn
226 275 280 285
229 Ala Ala Leu Ala Arg Ile Gln Thr Ile Ala Asp Ser Ala Gln Leu Val
230 290 295 300
233 Leu Thr Gly Asn Ser Gly Leu Ser Arg Ser Glu Gln Val Ala Gln Leu
234 305 310 315 320
237 Arg Glu Leu Ile Lys Gln Asn His Ser Glu Leu Val Gly Leu Glu Val
238 325 330 335
241 Ser His Ala Ser Leu Glu Leu Ile Lys Asn Lys Thr Glu Ser Phe Ala
242 340 345 350
245 Pro Asp Gln Leu Ala Thr Lys Leu Thr Gly Ala Gly Gly Gly Cys
246 355 360 365
249 Ala Val Thr Leu Leu Pro Asp Asp Phe Glu Glu Glu Lys Val Lys Glu
250 370 375 380
253 Leu Met Ser Glu Leu Glu Asn Ala Gly Phe Lys Cys Tyr Glu Thr Arg
254 385 390 395 400
257 Val Gly Gly Asp Gly Phe Gly Val Lys Leu Leu Gln Asp Glu Gln Glu
258 405 410 415
261 Glu Ala Glu Ala Lys Leu Arg Phe Lys Glu Ala Asn Val Ser Asn Glu
262 420 425 430
265 Leu Ala Val Trp Ala Asp Glu Leu Ala Gly Trp Val Phe Ala
266 435 440 445

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/562,472

DATE: 01/09/2006

TIME: 11:29:41

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01092006\J562472.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29
L:273 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2